

Amendments to the Specification:

Please replace the paragraph beginning at page 11, line 1 with the following amended paragraph:

The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See <http://www.ncbi.nlm.nih.gov>.

Please replace the paragraph beginning at page 26, line 5 with the following amended paragraph:

The "TCoA1" region locus was determined using Genebridge4 radiation hybrid panel of 91 hybrids (Walter et al. (1994) Nature Genetics 7:22-28). Screening was done by re-using primer-G and primer-H and performing PCR for that hybrid panel. By evaluating the respective hybrids as being positive or negative in regard to amplification, the binary code produced was compared with the similarity code for the marker that forms the framework map using the server at the web-address <http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl> to determine the chromosomal location of the gene of the invention. "TCoA1" recognized to be located in the marker D17S1557 (Fig. 2B). Only a score below 11 showing the possibility of "TCoA1" existing at a site away from D17S1557 was detected. This site coincides with the results by FISH showing FAC1 is on chromosome no. 17 q24 (Bowser (1996) Genomics 38:455-457).